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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/908,992

DATE: 01/31/2002
TIME: 15:55:08

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3 <110> APPLICANT: SYKEN, JOSH
4 MUNGER, KARL
6 <120> TITLE OF INVENTION: METHODS AND REAGENTS TO REGULATE APOPTOSIS
8 <130> FILE REFERENCE: HMV-054.01
10 <140> CURRENT APPLICATION NUMBER: 09/908,992
C--> 11 <141> CURRENT FILING DATE: 2002-01-09
13 <150> PRIOR APPLICATION NUMBER: 60/219,718
14 <151> PRIOR FILING DATE: 2000-07-19
16 <150> PRIOR APPLICATION NUMBER: 60/219,537
17 <151> PRIOR FILING DATE: 2000-07-20
19 <160> NUMBER OF SEQ ID NOS: 27
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2656
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (32)..(1471)
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35 1 5
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38 Arg Trp Leu Leu Val Val Val Gly Thr Pro Arg Leu Pro Ala Ile Ser
39 10 15 20
41 ggt aga ggg gcc cgg ccc agg gag ggc gtc gtt ggg gca tgg ctg 148
42 Gly Arg Gly Ala Arg Pro Pro Arg Glu Gly Val Val Gly Ala Trp Leu
43 25 30 35
45 agc cgc aag ctg agc gtc ccc gcc ttt gct tct tcc ctg acc tct tgc 196
46 Ser Arg Lys Leu Ser Val Pro Ala Phe Ala Ser Ser Leu Thr Ser Cys
47 40 45 50 55
49 ggc ccc cga gcg ctg ctg aca ttg aga cct ggt gtc agc ctt aca gga 244
50 Gly Pro Arg Ala Leu Leu Thr Leu Arg Pro Gly Val Ser Leu Thr Gly
51 60 65 70
53 aca aaa cat aac cct ttc att tgt act gcc tcc ttc cac acg agt gcc 292
54 Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser Phe His Thr Ser Ala
55 75 80 85
57 cct ttg gcc aaa gaa gat tat tat cag ata ttg gga gtc cct cga aat 340
58 Pro Leu Ala Lys Glu Asp Tyr Tyr Gln Ile Leu Gly Val Pro Arg Asn
59 90 95 100
61 gcc agc cag aaa gag atc aag aaa gcc tat tat cag ctt gcc aag aag 388
62 Ala Ser Gln Lys Glu Ile Lys Ala Tyr Tyr Gln Leu Ala Lys Lys

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65	tat cac cct gac aca aat aag gat gat ccc aaa gcc aag gag aag ttc	436		
66	Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Lys Ala Lys Glu Lys Phe			
67	120	125	130	135
69	tcc cag ctg gca gaa gcc tat gag gtt ttg agt gat gag gtg aag agg	484		
70	Ser Gln Leu Ala Glu Ala Tyr Glu Val Leu Ser Asp Glu Val Lys Arg			
71	140	145	150	
73	aag cag tac gat gcc tac ggc tct gca ggc ttc gat cct ggg gcc agc	532		
74	Lys Gln Tyr Asp Ala Tyr Gly Ser Ala Gly Phe Asp Pro Gly Ala Ser			
75	155	160	165	
77	ggc tcc cag cat agc tac tgg aag gga ggc ccc act gtg gac ccc gag	580		
78	Gly Ser Gln His Ser Tyr Trp Lys Gly Gly Pro Thr Val Asp Pro Glu			
79	170	175	180	
81	gag ctg ttc agg aag atc ttt ggc gag ttc tca tcc tct tca ttt gga	628		
82	Glu Leu Phe Arg Lys Ile Phe Gly Glu Phe Ser Ser Ser Phe Gly			
83	185	190	195	
85	gat ttc cag acc gtg ttt gat cag cct cag gaa tac ttc atg gag ttg	676		
86	Asp Phe Gln Thr Val Phe Asp Gln Pro Gln Glu Tyr Phe Met Glu Leu			
87	200	205	210	215
89	aca ttc aatcaa gct gca aag ggg gtc aac aag gag ttc acc gtg aac	724		
90	Thr Phe Asn Gln Ala Ala Lys Gly Val Asn Lys Glu Phe Thr Val Asn			
91	220	225	230	
93	atc atg gac acg tgt gag cgc tgc aac ggc aag ggg aac gag ccc ggc	772		
94	Ile Met Asp Thr Cys Glu Arg Cys Asn Gly Lys Gly Asn Glu Pro Gly			
95	235	240	245	
97	acc aag gtg cag cat tgc cac tac tgt ggc ggc tcc ggc atg gaa acc	820		
98	Thr Lys Val Gln His Cys His Tyr Cys Gly Ser Gly Met Glu Thr			
99	250	255	260	
101	atc aac aca ggc cct ttt gtg atg cgt tcc acg tgt agg aga tgt ggt	868		
102	Ile Asn Thr Gly Pro Phe Val Met Arg Ser Thr Cys Arg Arg Cys Gly			
103	265	270	275	
105	ggc cgc ggc tcc atc atc ata tcg ccc tgt gtg gtc tgc agg gga gca	916		
106	Gly Arg Gly Ser Ile Ile Ile Ser Pro Cys Val Val Cys Arg Gly Ala			
107	280	285	290	295
109	gga caa gcc aag cag aaa aag cga gtg atg atc cct gtg cct gca gga	964		
110	Gly Gln Ala Lys Gln Lys Lys Arg Val Met Ile Pro Val Pro Ala Gly			
111	300	305	310	
113	gtc gag gat ggc cag acc gtg agg atg cct gtg gga aaa agg gaa att	1012		
114	Val Glu Asp Gly Gln Thr Val Arg Met Pro Val Gly Lys Arg Glu Ile			
115	315	320	325	
117	ttc att acg ttc agg gtg cag aaa agc cct gtg ttc cgg agg gac ggc	1060		
118	Phe Ile Thr Phe Arg Val Gln Lys Ser Pro Val Phe Arg Arg Asp Gly			
119	330	335	340	
121	gca gac atc cac tcc gac ctc ttt att tct ata gct cag gct ctt ctt	1108		
122	Ala Asp Ile His Ser Asp Leu Phe Ile Ser Ile Ala Gln Ala Leu Leu			
123	345	350	355	
125	ggg gga aca gcc aga gcc cag ggc ctg tac gag acg atc aac gtg acg	1156		
126	Gly Gly Thr Ala Arg Ala Gln Gly Leu Tyr Glu Thr Ile Asn Val Thr			
127	360	365	370	375

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130 Ile Pro Pro Gly Thr Gln Thr Asp Gln Lys Ile Arg Met Gly Gly Lys		
131 380	385	390
133 ggc atc ccc cgg att aac agc tac ggc tac gga gac cac tac atc cac		1252
134 Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr Gly Asp His Tyr Ile His		
135 395	400	405
137 atc aag ata cga gtt cca aag agg cta acg agc cgg cag cag agc ctg		1300
138 Ile Lys Ile Arg Val Pro Lys Arg Leu Thr Ser Arg Gln Gln Ser Leu		
139 410	415	420
141 atc ctg agc tac gcc gag gac gag aca gat gtg gag ggg acg gtg aac		1348
142 Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp Val Glu Gly Thr Val Asn		
143 425	430	435
145 ggc gtc acc ctc acc agc tct ggt ggc agc acc atg gat agc tcc gca		1396
146 Gly Val Thr Leu Thr Ser Ser Gly Gly Ser Thr Met Asp Ser Ser Ala		
147 440	445	450
149 gga agc aag gct agg cgt gag gct ggg gag gac gag gag gga ttc ctt		1444
150 Gly Ser Lys Ala Arg Arg Glu Ala Gly Glu Asp Glu Glu Gly Phe Leu		
151 460	465	470
153 tcc aaa ctt aag aaa atg ttt acc tca tgatatccca gccgaggaaa		1491
154 Ser Lys Leu Lys Lys Met Phe Thr Ser		
155 475	480	
157 aagatccact ggaaacttagg ccgggaagca gcagccccctc caagggccag ggcacctggg		1551
159 agacgggagg attccagaac agcagcactg agctccccacc cgcagacgc ctggacggcc		1611
161 ttggcaacac caaaatcatg ggacaaacacc tctctccacg gaaaggtcac agtggacagc		1671
163 ccggcagta ggatgcagcc ccagaggctg gtggcagtt cctgtccatt gtaggtgac		1731
165 ggccccctgg tcagcagagg agaggttaga tcttcagggc taaaactcta atttggaaatt		1791
167 gaatattgtg gatatcttag ttaaaggcca tgcttacagc ttagaaatga agcctaagc		1851
169 tgcataagt tacgaagtga ttaatttcct tctcagcaaa cctccggag gttccagaat		1911
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173 cgtcctccccc taatgagggg ccctgccgag gcatcagctg ctctgctcgt ttagtttta		2031
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179 ttgctccac cccatccggg atggccgcct gtccctgact attgagtcct gttgtgtaa		2211
181 gcccaggcatg gagggtctcct gcccctctgc tgagccacag cccattgcag cactgtcgt		2271
183 gcccaggacttc agctgccttg ggaactgaag ccctgccact gttgctagtc aggggcttgg		2331
185 ttctcccact tacactgttg acatctattt tctgaagtgt gtttaaattt ttcagtgcata		2391
187 atcattgtttt ttccctttgtt aatgttgat tcagaaaagg aaagcacagg ctaagcagtt		2451
189 gaagggttccc caccatttcag tgagagcaga acccccattc cccagccctc gctggtagca		2511
191 tgcgcagtt tccatgtgtt tcaggatctt cgggctgtcg ttagacaggt taatgaagaa		2571
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209	Met	Ala	Ala	Arg	Cys	Ser	Thr	Arg	Trp	Leu	Leu	Val	Val	Val	Gly	Thr	
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212	ccg	cg	ctg	ccg	gct	ata	tcg	ggt	aga	gg	gcc	cg	ccg	ccc	agg	gag	96
213	Pro	Arg	Leu	Pro	Ala	Ile	Ser	Gly	Arg	Gly	Ala	Arg	Pro	Pro	Arg	Glu	
214						20				25					30		
216	ggc	gtg	gtg	gg	gca	tgg	ctg	agc	cg	aag	ctg	agc	gtc	cc	gcc	ttt	144
217	Gly	Val	Val	Gly	Ala	Trp	Leu	Ser	Arg	Lys	Leu	Ser	Val	Pro	Ala	Phe	
218						35			40						45		
220	g	c	t	t	c	t	cc	ct	tc	gg	cc	cg	ct	ct	ac	tt	192
221	Ala	Ser	Ser	Leu	Thr	Ser	Cys	Gly	Pro	Arg	Ala	Leu	Leu	Thr	Leu	Arg	
222						50			55			60					
224	cct	gg	gt	tc	ag	ct	tt	ac	gg	aa	ca	aa	ca	tt	tg	at	240
225	Pro	Gly	Val	Ser	Leu	Thr	Ser	Cys	Gly	Pro	Arg	Ala	Leu	Leu	Thr	Leu	Arg
226						65			70			75				80	
228	gg	cc	tcc	ttc	cac	ac	gt	gg	cct	tt	gg	aa	aa	gat	ta	ta	288
229	Ala	Ser	Phe	His	Thr	Ser	Ala	Pro	Leu	Ala	Lys	Glu	Asp	Tyr	Tyr	Gln	
230						85				90					95		
232	at	at	tt	gg	gt	cc	tt	cg	aa	gg	at	cc	aa	gg	aa	cc	336
233	Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Asp	Tyr	Tyr	Gln	
234						100			105			110					
236	ta	ta	c	tt	gg	aa	gg	aa	tt	cc	tc	g	ac	aa	gg	at	384
237	Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	
238						115			120			125					
240	cc	aa	gg	aa	gg	aa	tt	cc	tg	ca	gg	aa	gg	tt	at	gg	432
241	Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val	
242						130			135			140					
244	tt	tg	ag	tg	aa	gg	aa	gg	ca	tt	gg	cc	tt	tg	ca	480	
245	Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala	
246						145			150			155			160		
248	gg	cc	tcc	gg	gg	cc	ag	gg	tcc	ca	cat	ag	tc	tg	aa	gg	528
249	Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	
250						165				170					175		
252	gg	cc	576														
253	Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	
254						180			185			190					
256	tt	tc	624														
257	Phe	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro		
258						195			200			205					
260	ca	ga	ta	tc	at	g	tg	tt	ca	tt	ca	gg	tt	ca	gg	tt	672
261	Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val	
262						210			215			220					
264	aa	aa	gg	tt	cc	tt	cc	tt	cc	tt	ca	gg	tt	ca	gg	tt	720
265	Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	
266						225			230			235			240		
268	gg	cc	aa	gg	cc	cc	gg	cc	aa	gg	tt	ca	tt	ca	tt	768	
269	Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	
270						245			250			255					
272	gg	gg	tcc	gg	tt	cc	at	gg	cc	tt	ca	gg	cc	tt	tg	at	816

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273	Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg		
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276	tcc	acg	tgt	agg	aga	tgt	ggt	ggc	cgc	ggc	tcc	atc	atc	ata	tcg	ccc	864	
277	Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro		
278			275					280							285			
280	tgt	gtg	gtc	tgc	agg	gga	gca	gga	caa	gcc	aag	cag	aaa	aag	cga	gtg	912	
281	Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val		
282			290					295							300			
284	atg	atc	cct	gtg	cct	gca	gga	gtc	gag	gat	ggc	cag	acc	gtg	agg	atg	960	
285	Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met		
286	305				310						315				320			
288	cct	gtg	gga	aaa	agg	gaa	att	ttc	att	acg	ttc	agg	gtg	cag	aaa	agc	1008	
289	Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser		
290				325						330					335			
292	cct	gtg	ttc	cgg	agg	gac	ggc	gca	gac	atc	cac	tcc	gac	ctc	ttt	att	1056	
293	Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile		
294				340				345							350			
296	tct	ata	gct	cag	gct	ctt	ctt	ggg	gga	aca	gcc	aga	gcc	cag	ggc	ctg	1104	
297	Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu		
298				355				360							365			
300	tac	gag	acg	atc	aac	gtg	acg	atc	ccc	cct	ggg	act	cag	aca	gac	cag	1152	
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302				370				375							380			
304	aag	att	cgg	atg	ggt	ggg	aaa	ggc	atc	ccc	cgg	att	aac	agc	tac	ggc	1200	
305	Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly		
306	385				390				395						400			
308	tac	gga	gac	cac	tac	atc	cac	atc	aag	ata	cga	gtt	cca	aag	agg	cta	1248	
309	Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu		
310					405					410					415			
312	acg	agc	cgg	cag	cag	agc	ctg	atc	ctg	agc	tac	gcc	gag	gac	gag	aca	1296	
313	Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr		
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316	gat	gtg	gag	ggg	acg	gtg	aac	ggc	gtc	acc	ctc	acc	agc	tct	ggt	ggc	1344	
317	Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Gly		
318					435				440						445			
320	agc	acc	atg	gat	agc	tcc	gca	gga	agc	aag	gct	agg	cgt	gag	gct	ggg	1392	
321	Ser	Thr	Met	Asp	Ser	Ser	Ala	Gly	Ser	Lys	Ala	Arg	Arg	Glu	Ala	Gly		
322					450			455							460			
324	gag	gac	gag	gag	gga	tcc	ctt	tcc	aaa	ctt	aag	aaa	atg	ttt	acc	tca	1440	
325	Glu	Asp	Glu	Glu	Gly	Phe	Leu	Ser	Lys	Leu	Lys	Lys	Met	Phe	Thr	Ser		
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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date